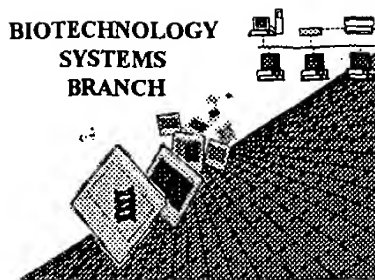


0300

RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/863,600A

Source: O/PE

Date Processed by STIC: 11/12/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

| ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 09/863600A |
|--|--|---------------------------|
| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | | |
| 1 ___ Wrapped Nucleics ___ Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." | |
| 2 ___ Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. | |
| 3 ___ Misaligned Amino ___ Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. | |
| 4 ___ Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. | |
| 5 ___ Variable Length | Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. | |
| 6 ___ PatentIn 2.0 ___ "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. | |
| 7 ___ Skipped Sequences ___ (OLD RULES) | Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. | |
| 8 ___ Skipped Sequences ___ (NEW RULES) | Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000 | |
| 9 ___ Use of n's or Xaa's ___ (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. | |
| 10 ___ Invalid <213> ___ Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence | |
| 11 J ___ Use of <220> | Sequence(s) 49 (maybe more) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) | |
| 12 ___ PatentIn 2.0 ___ "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. | |
| 13 ___ Misuse of n | n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide. | |

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/863,600A

DATE: 11/12/2001

TIME: 18:31:16

Input Set : A:\es.txt

Output Set: N:\CRF3\11122001\I863600A.raw

4 <110> APPLICANT: Smith-Swintosky, Virginia
 5 Renzi, Michael
 6 Plata-Salaman, Carlos
 7 Jolliffe, Linda
 8 Farrell, Francis
 9 Johnson, Dana
 11 <120> TITLE OF INVENTION: Neuroprotective Peptides
 13 <130> FILE REFERENCE: ORT1436
 15 <140> CURRENT APPLICATION NUMBER: 09/863,600A
 16 <141> CURRENT FILING DATE: 2001-05-23
 18 <160> NUMBER OF SEQ ID NOS: 49
 20 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
 Corrected Diskette Needed

ERRORED SEQUENCES

822 <210> SEQ ID NO: 49
 823 <211> LENGTH: 12
 824 <212> TYPE: PRT
 825 <213> ORGANISM: Artificial Sequence
 827 <220> FEATURE:
 828 <221> NAME/KEY: variant
 829 <222> LOCATION: 1, 2, 3, 4, 5, 8, 11, 12
 830 <223> OTHER INFORMATION: Description of Artificial Sequence: 1 is D-Tyr, p-NO₂-Phe,
 p-NH₂-Phe, p-F-
 831 Phe, p-I-Phe, or 3,5-dibromo-Tyr, 2 and 8 is any L or D amino acid, 3 is Cys,
 832 Glu, Ala, (-amino-(-bromobutyric acid, or homocysteine, 4 is Arg, His, Tyr,
 Leu,
 833 or Trp, 5 is Phe, Met, or Ile, 12 is Cys, Lys, Ala, (-amino-(-bromobutyric
 acid,
 W--> 834 or homocysteine, 11 is Asp, Glu, Val, Ile, or Leu
 836 <400> SEQUENCE: 49
 W--> 837 Xaa Xaa Xaa Xaa Xaa Gly Pro Xaa Thr Trp Xaa Xaa
 838 1 5 10
 E--> 840 15
 E--> 842 15 delete

<223> response
 This does not explain
 source of genetic material -
 see item 11 on Error
 summary sheet

Per 1.823 d
 Sequence Rules,

<223> response
 cannot exceed 4 lines

first Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 11/12/2001

PATENT APPLICATION: US/09/863,600A

TIME: 18:31:17

Input Set : A:\es.txt

Output Set: N:\CRF3\11122001\I863600A.raw

L:37 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:74 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:91 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:110 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:623 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
L:659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:677 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41
L:713 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:731 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:802 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:818 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48
L:834 M:259 W: Allowed number of lines exceeded, <223> Other Information:
L:837 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49
L:840 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:49
M:332 Repeated in SeqNo=49